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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a
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11406.588 Million cell updates/sec
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Gapop_60.0 , Gapext 60.0
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 BD196412 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL		0 C	4.	4.	4.4	. ω	ω	c 37	Ju	υ	w	c 321	, w	N	o n	) N	N	C 22	งง	N	N ⊢	۰,	Д,	0 L5	. ب	<u> </u>				ი თ -	<b>J</b> 0	·Ω		0 U K	, <sub>L</sub>	No. S	ל ( הפסון ל
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OS Homo sepiens (human)

PN 17 200216657-A/1

PD 11-UNE-2002

PF 20-DEC-1999 UP 200022562

PF 22-DEC-1999 UP 200022562

PF 22-DEC-1999 US 06/996366,99-SEP-1998 US 60/099658 PT

DANIEL COHEN, MARTA BILMENFELD, ILYA CHUMAKOV, LYDIE BOUGHLERET PC

CINNIS/00,C12NS/00, DOIXK9/027,C07X4/47.C07X6/18.120N1/35.9 PC

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RESULT 2 BD196564 LOCUS DEFINITION ACCESSION VERSION VERSION ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	B 6	Ъ
BD19654 Series and Series by DNA linear PAT 17-JUL-2003 BD19654.1 GI:33006334 JP 2002516567-A/153. Homo aspiens (human) ENKRYPCE; Mecazos; Chordate; Craniate; Vertebrate; Enteleostomi; Homo aspiens (human) Homo aspiens	1081 AACTTAAGTTCTCGTGAT 1098 	

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CC upstream amplification primer 4-67, complement CC amplification primer 5-50 complement CC CC downstream amplification primer 5-50, complement C upstream amplification primer 5-71 CC downstream amplification primer 5-71
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CC downstream amplification primer 99-21
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polyA\_signal
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exon polyA

Qy 1 GTTTCTTGTTCCTGCATTTTTATTTTTATTGTATGGAGGGACAAATAATTATTTTCTGT 60	Query Match 100.0%; Score 1098; DB 6; Length 56520; Best Local Similarity 100.0%; Pred. No. 0; Matches 1098; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	primer_bind 51772. primer_bind 52199.	primer_bind 51667. primer_bind 51387. primer_bind 51826.	primer_bind 51593. primer_bind 29734. primer_bind 51167.	primer bind 50774. primer bind 51183. primer bind 51186. primer bind 51146.	FT primer bind 50541. 50560 FT primer bind 5094050959 FT primer bind 5055550572	primer bind 49331. primer bind 49830. primer bind 50271. primer bind 50172.	primer bind 47879. primer bind 47879. primer bind 48217. primer bind 48902.	primer bind 40629. primer bind 40629. primer bind 41058. primer bind 45729.	primer bind 35182. primer bind 39591. primer bind 39971. primer bind 40531.	34624. 34473. 34916. 34702.	primer bind 27022. primer bind 32262. primer bind 32823. primer bind 34215.	primer_bind 23111. primer_bind 25098. primer_bind 25657. primer_bind 26537.	primer bind 18699. primer bind 19164. primer bind 22589.	primer_bind 16463. primer_bind 17304. primer_bind 17814. primer_bind 18008.	primer_bind 13617. primer_bind 13547. primer_bind 13962. primer_bind 15994.	primer_bind 12339. primer_bind 12915. primer_bind 13317. primer_bind 13216.	<pre>primer_bind 11622. primer_bind 12018. primer_bind 11930.</pre>
Db 4979 AACTTAAGTTCTCGTGAT 4996	4919 1081	Db 4859 GACTATTGAAAATCCAGTTAAGTCTCTCTCTACTGTGTTGAGAGGCATTGATTCAAGTACCT 4918  OY 1021 GTGTTACTTTCCTGTGCTGCCAAAACAGATCACCTCAAACTAAGCGGCTTAAAATAATAG 1080	GACTATTGAAAATCCAGTTAAGTCTCTCTACTGTGTTGAGAGGCATTGATTCAAGTACCT 102	Qy 901 TATTTCTTTAGAATAAGTAATAAGAATTTTATAAGCTTTTTTATATTTCACGTAATTTGA 960	o 4	<b>a</b> 4	Oy 721 TCTGGGTAAATACCTTTTTCTTCCCCAGTTTCACTACTTTATTTTCATATGTATCTCTGA 780	OY 661 ATGATCTGTGCTTGGCAGGTAAACCTGCTTCCAACAAATTTAGTTGGATTTTTCTTGGAT 720	Oy 601 TATTTTCTTTTACATAGAATTTTTAAGCTGAAGAGAAGTAGTAGTAGGTCCATGAGATTT 660	Qy 541 TTACACCTTTCAACTCTAGGTTTAAAAAATAAGTGGTTCACAGTAGTTCTTGCAGAAGAA 600	Qy 481 TTATTAATTATATATATATATATAAAGAGGCATTTTAAAATAAAATTTTTTTAAATGACATTT 540	Oy 421 GACTCATTTCTGAAGGGAGTTTTAGTAATTTAAGAGGTTATAAGTTTTTAAATAAAGGT 480	QY 361 TTTATCAGCTTTCGTTTGCAAGGCTAGTGATGATCTCTCTGTTCTGTATAAAGTATTGTT 420	Oy 301 TTAAAATTTTTAGCTTGCTTTTCTTGTTTAGGACACTCTTTTTTTCTTGAATTGTT 360	- QY 241 TGTCACCTTATTTTTACCTGTGACTTTGTACCATTAACTTTGTCACTGAGATGTTTTGA 300	QY 181 AGGAATAAATAGCTATCTTCAAACATAAGACCCAAAGGAAAAAGATTTATAGTGATGTTC 240	QY 121 TGTGTACACAAAGCTAĆCTTTCAATATTTTTTTTTTTTTT	Qy 61 TTAGTAACAGAGCAGGTATTTTGAATTTATTAGGGTCTTTTTCTGCAGTCTGGGTTTCC 120

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA CB (bases 1 to 165799)

E3 (bases 1 to 165799)

RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Norman, C.H., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teefay, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                  Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17048183. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Nusbaum,C. and Lander,E.

Birren,B., Nusbaum,C. and Lander,E.
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_CANCELLED
Homo sapiens (human)
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Mammalia; Eutheria; Primates;
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Homo sapiens chromosome 8 clone CTD-2541M15 map 8, 4 unordered
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                                                                                                             Center: Whitehead Institute/ MIT Center
Contact: sequence_submissions@genome.wi.mit.edu
                                    Web site: http://www-seq.wi.mit.edu
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                   TTACACCTTTCAACTCTAGGTTTAAAAAATAAGTGGTTCACAGTAGTTCTTGCAGAAGAA
                                                                 TTATTAATTTATATATATAAAGAGGCATTTTAAAATAAAATTTTTTTAAATGACATTT
                                                                                    GACTCATTTCTGAAGGGAGTTTTAGTAATTTAAGAGGTTATAAGTTTTTAAATAAAGGT
                                                                                                                                                                GACTCATTTCTGAAGGGAGTTTTAGTAATTTAAGAGGTTATAAGTTTTTAAATAAAGGT
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Center project name: L21488
Center clone name: 2541_M_15
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/clone_lib="CITD2 Human BAC"
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mol_type="genomic DNA"
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1 (bases 1 to 168136)
Reichwald, K., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N., Menzel, U., Polley, A., Schilhabel, M.B., Taudien, S., Wen, G. and Rosenthal, A.
                                    Biotechnology, Beutenberstr. 11, 5 (bases 1 to 168136)
                                                                                                         Biotechnology, Beutenberstr. 4 (bases 1 to 168136)
Lagemann, D. and Platzer, M.
                                                                                                                                                      Submitted (23-AUG-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany
                                                                                                                                                                                                                    3 (bases 1 to 168136)
Reichwald, K. and Platzer, M.
                                                                                                                                                                                                                                                             Submitted (14-JUL-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                        Genome Sequencing Center Jena.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Lagemann, D. and
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Submitted (09-JUL-2002) Genome Analysis, Institute of Submitted (09-JUL-2002) Genome Analysis, Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Suomission.
Submitted (03-ARR-2002) Genome Analysis, Institut
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Lagemann, D. and Platzer, M. Direct Submission
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Lagemann, D. and Platzer, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Quality Assessment:
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This clone is overlapped by GS1-24F4, GS1-24F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality levels above 40 are expected to have less 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Insitute of Molecular Biotechnology Center code: IMB Web site: http://genome.imb-jena.de/Contact: gscj-submit@genome.imb-jena.de
------ Project Information
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Center project name: H351
Center clone name: CTD-2541M15
                                                  28243.
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                                                                                                                                                                                                  organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                           note="single"
                                                  /note="single stranded/single chemistry region"
28243. .28507
                                                                                                               note="low quality region"
                                                                                                                                                           note="overlapping clone, overlapping"
                                                                                                                                                                               clone="GS1-24F4"
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db_xref="taxon:9606"
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huringia 07745, Germany
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                     Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2001 this sequence version replaced gi:12313816. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1 (bases 1 to 183485)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens, clone RP11-15C20
                                                                                                                                                                                                                                             Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                             Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC022578.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATAGAGAAATATTTCAGTCAGTGCTAAAATTGTTCCTTATAACTCGTTTATCCTTT 116904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACTTAAGTTCTCGTGAT 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGTTACTTTCCTGTGCCAAAACAGATCACCTCAAACTAAGCGGCTTAAAATAATAG 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATTTCTTTAGAATAAGTAATAAGAATTTTATAAGCTTTTTTATATTTCACGTAATTTGA 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGGTCCTTCCAGAATCTCTCATTGGTACTGAAACTCAAATGGGTACTTTCTTCACCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATAGAGAAATATTTCAGTCAGTGCTGCTAAAATTGTTCCTTATAACTCGTTTATCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGGGTAAATACCTTTTTCTTCCCCAGTTTCACTACTTTATTTTCATATGTATCTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACTTAAGTTCTCGTGAT 117162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGTTACTTTCCTGTGCTGCCAAAACAGATCACCTCAAACTAAGCGGCTTAAAATAATAG 117144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTATTGAAAATCCAGTTAAGTCTCTCTACTGTGTTGAGAGGCATTGATTCAAGTACCT 117084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 183485)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2578 183485 bp DNA linear HTG 16-MAR-2001 sapiens clone RP11-15C20, WORKING DRAFT SEQUENCE, 11 unordered
Institute/ MIT Center
       for
       Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid; n/a; 96% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0,960731 Consensus quality: 179658 bases at least 040 Consensus quality: 181356 bases at least Q30 Consensus quality: 181356 bases at least Q30 Consensus quality: 182011 bases at least Q20 Insert size: 170000; agarose-fp Insert size: 182485; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
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Center clone name: 15_C_20
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67158. .126278
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9 126278: contig of 59121 bp
9 126378: gap of 100 bp
9 183485: contig of 57107 bp
Location/Qualifiers
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43876. .67057
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db_xref="taxon:9606"
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14380: gap of
25807: contig
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43975: contig of 17868 bp
43875: gap of 100 bp
67057: contig of 23182 bp
67157: gap of 100 bp
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ig of 2767 bp in length
of 100 bp
ig of 2442 bp in length
of 100 bp
ig of 4247 bp in length
of 100 bp
of 100 bp
of 100 bp
ig of 11427 bp in length
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100 bp
of 1051 bp in length
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of 1886 bp in length
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	01 TATTTCTTTAGAATAAGTAATAAGAATTTTATAAGCTTTTTTATATTTCACGTAATTTGA 960 	Qy
058		Db 769
998	9 GATAGAGAAATATTTCAGTCAGTGCTGCTAAAATTGTTCCTTATAACTCGTTAITA	769
	1 GATAGAGAAAATATTTCAGTCAGTGCTGCTAAAAATTGTTCCTTATAACTCGTTTATCCCTTT 84	7
93.8	21 TCTGGGTAAATACCTTTTTCTTCCCCAGTTTCACTACTTATTTTCATATGTATCTCTGA 780 	Qy 72 Db 7687
378	61 ATGATCTGTGCTTGGCAGGTAAACCTGCTTCCAACAAATTTAGTTGGATTTTTCTTGGAT 720 	Qy 66 Db 7681
818	1 TATTTTCTTTTACATAGAATTTTTAAGCTGAAGAAGTAGTAGTAGGTAG	Qy 60 Db 7675
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88	31 TTATTAATTTATATATATATAAAGAGGCATTTTAAAATAAAATTTTTTTT	Qy 48 Db 7663
53 8	21 GACTCATTTCTGAAGGGAGTTTTAGTAATTTAAGAGGTTATAAGTTTTTAAATAAAAGGT 480 	Qy 42 Db 7657
578	51 TTTATCAGCTTTCGTTTGCAAGGCTAGTGATGATCTCTTGTTCTGTATAAAGTATTGTT 420 	Qy 36 Db 7651
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338	21 TGTGTACACAAAGCTACCTTTCAATATTTTTATTGTTTCTGTTAAGATTAAATCAATAG 180 	Qy 12 Db 7627
278	SI TTAGTAACAGAGCAGGGTATTTTGAATTTATTAGGGTCTTTTTCTGCAGTCTGGGTTTTCC 120	Qy 6 Db 7621
8 .	1 GITTCTIGITCCIGCATITTTATITTATIGTATGGAGGGACAAATAATTATTITCTGI 60	Qy Db 7615
<i></i>	th 90.7%; Score 996; DB 2; Length 183485;   Similarity 99.8%; Pred. No. 0;   Conservative 0; Mismatches 2; Indels 0; Gaps 0	Query Match Best Local Matches 109
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	JOURNAL REFERENCE AUTHORS	TITLE	REFERENCE AUTHORS TITLS JOURNAL REFERENCE AUTHORS	RESULT 6 AC091099 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 108 Db 7723	Qy 1021 Db 77179		Db 77059
Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H.,	(29-MAR-2001) Whitehead Institute/MIT Center for C 320 Charles Street, Cambridge, MA 02141, USA 1 to 209718)  Nusbaum, C., Lander, E., Ali, A., Allen, N., Andersor	am, L., ue, K., Liu, G., Liu, G., McCarthy, M McCarthy, M Mcnorth, J., C., Norbu, Roman, J., Roman, J., Ck, R., Seam N., J., Tesfay assillev, H.	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 209718)  Birren, B., Nusbaum, C. and Lander, E.  Homo sapiens chromosome 8, clone RP11-782N1  Unpublished  2 (bases 1 to 209718)  Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,  Barria, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A.,  Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M.,  Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K.,  Diaz. J. C. Cooke, P., DeArellano, K., Dewar, K.,  Diaz. J. C. Cooke, P., DeArellano, K., Dewar, K.,  Diaz. J. C. Cooke, P., Devreira D. Fitzinch W. Goge D.	209718 bp DNA romosome 8 clone RP11-782 ordered pieces. 22122960 th Tros Protest (Transaction of the contest of	AACTTAAGTTCTCGTGAT 1098 	1 GTGTTACTTTCCTGTGCTGCCAAAACAGATCACCTCAAACTAAGCGGCTTAAAATAATAG 1080 	GACTATTGAAAATCCAGTTAAGTCTCTCTACTGTGTGAGAGGCATTGATTCAAGTACCT 	9 TATITCTTTAGAATAAGTAATAAGAATTTTATAAGCTTTTTTATATTTTCACGTAATTTGA 77118

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FEATURES
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JOURNAL
                misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Assembly program: Phrap; version 0.960731 (Consensus quality: 207012 bases at least Q40 (Consensus quality: 207712 bases at least Q30 (Consensus quality: 208339 bases at least Q20 Insert size: 205000; agarose-fp (Duality coverage: 8.8 in Q20 bases; agarose-fp quality coverage: 8.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of 100 bp
contig of 56040 bp in length
gap of 100 bp
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100 bp
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of 15875 bp in length
100 bp
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of 15152 bp in length
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of 8569 bp in length
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100 bp
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/note="assembly_fragment"
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152290. .208329
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Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C.,
Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,
Hagos, B., Heaford, A., Horton, L., Howland, J. C., Jones, C., Kann, L.,
Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P.,
Karatas, A., Lehoczky, J., Lieu, C., Locke, K., McLaughlin, J.,
Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,
Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J.,
Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Parlin, B.,
Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wu, X., Wyman, D., Ye, W. J., and Zody, M.
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                                                                                                                                         Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141 USA On Jul 7, 2000 this sequence version replaced gi:5932606.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBA
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1 (Dases 1 to 185834)

Birren,B., Linton,L., Nusbaum,C. and Lander,B.
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Homo sapiens chromosome 8 clone RP11-397K22
IN PROGRESS ***, 48 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2099
Center clone name: 397_K_22
                                                                                                                    Web site: http://www-seq.wi.mit.edu
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2 map 8, *** SEQUENCING
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NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-397K22
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be preserved.
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------ Project Information
Center project name: L2099
Center clone name: 397_K_22
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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158712: contig of 7958 bp in length
158812: gap of 100 bp
168916: contig of 10104 bp in length
169016: gap of 100 bp
185834: contig of 16818 bp in length.
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/db_xref="taxon:32630"
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Muzny, D. Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Coxkrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Duyan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
                                                                                                                                                                                                                                                                                                                                                                   AC135128.
AC135128.2 GI:25138667
HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264864 bp DN Rattus norvegicus clone CH230-249F17, ***, 2 unordered pieces. AC13517e
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Parkway, St. Louis, MO 6
On Dec 12, 2003 this sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-SEP-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: M_BB0186D01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: submissions@watson.wustl.ed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site:http://genome.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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The sequence of Mus musculus clone
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12, 2003 this sequence version replaced gi:23322797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (003) Genome Sequencing Center, 4444 Forest MO 63108, USA
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SEQUENCING IN PROGRESS
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REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

COMMENT

Center project name: Center clone name: CH Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Project Information

Center: Baylor Co Center code: BCM

College of Medicine

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Manhjum, S., Maghar, F., Martin, N., Martin, R., Manhjum, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Munidasa, M., Murphy, M., Nair, L., Morgan, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Morgan, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Morgan, M., Morris, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul.-L., Plopper, F., Poindexter, A., Rose, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Suton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walter, R., Walker, B., Wang, J., Walter, R., Walter, R., Walte, P., Wang, Q., Wang, S., Willson, R., Wilson, R., Weiss, R., Wooden, H., Worley, K., Wilson, J., Zhou, J., Zhou, J., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, D.R
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                                                                                                                                                                                                                           Submitted (20 NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 20, 2002 this sequence version replaced gi:23507717.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                     may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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      shotgun sequence
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only contigs will be indicated in the feature
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                                                          1 (bases 1 to 47)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 1768 25-MAR-2003;
                                                                                                                                                                              Unknown
                                                                                                                                                                                                                                                             Sequence 1768 from patent AR290033
                                                                                                                                                                                                                                                                                                    AR290033
                                                                                                                                                             Unclassified.
                                                                                                                                                                                                     Unknown.
                                                                                                                                                                                                                                            AR290033.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hggc.bcm.tmc.edu/docs/Genbank draft data.h NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                      AATATTTCTTTTACATAGAATTT 195495
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263405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%; Score 24; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end_sequence:BZ213258"
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/note="clone_boundary
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                                     Location/Qualifiers
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 263304: contig of 263304 bp in length
5 263404: gap of unknown length
5 264864: contig of 1460 bp in length.
Location/Qualifiers
/organism="unknown"
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AXI14392
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                                                                                                                                                                                                                                                        Sequence 132 from Patent AX281468 AX281468.1 GI:16608723
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE AUTHORS TITLE JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Nammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 56516)
Cohen,D., Blumenfeld,M., Chumakov,I. and Prostatic cancer gene
Patent: JP 2002516657-A 1 11-JUN-2002;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Bougueleret, L.

RESULT 1
BD196412
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD196412
Prostatic cancer gene.
BD196412
BD196412.1 GI:33006182
JP 2002516657-A/1.
Homo sapiens (human)
Homo sapiens

56516

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17-JUL-2003

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Result No. Score 1447 Query Match 212007 224600 247570 12029 108277 110000 159453 187241 2000 165799 168136 183485 209718 185834 Length 1095 1763 5226 5227 704 4682 4863 4932 4958 BB BX255915 BX510317 AL772146 AC127814 AR375789 AC23530 AX268078 BD196515 BD196514 BD196511 BD196513 BD196513 BD196517 BD196517 BD196510 BD196520 BD196520 BD196520 BD196520 BD196521 BD196521 BD196520 BD196521 BD196520 BD196521 BD196520 BD196521 BD196520 BD196521 BD196520 BD196521 BD196520 BD196520 BD196520 BD196520 BD196521 AX268080 AX339146 BD196448 BD196488 BD19648 AC009632 AX141275 AC022578 AC091099 AC100813 AF287957 ij SUMMARIES ALIGNMENTS AX268078 BD196515 BD196497 BD196514 BD196511 BD196513 BD196518 BD196518 BD196512 BD196520 BD196510 BD196516 BD196516 BD196521 AX2136808 AR339146 BD196448 BD196448 BD196448 BD196418 BD196418 AX869838 BD196418 AX869838 BD196418 AX869838 BD196418 AX869838 BD196418 BD196418 AX869838 BD196418 AX869838 BD196418 AX869838 BD196418 BD196418 AX869838 BD196518 AX869838 AX869838 AX86988 BD196518 AX86988 BX255915 AX877214 AC091099 AC009632 AX141275 Description Homo sapi Homo sapi Sequence Prostatic Homo sapi Homo sapi Homo sapi Sequence Sequence Primer for Homo sapi Rattus no Rattus no Rattus no Plasmodiu Lotus cor Danio rer Zebrafish Rattus no Rattus no positiva cor Sebrafish Rattus no Prostatic Homo sapi Sequence Sequence Prostatic Prostatic Sequence Primer fo Homo sapi Prostatic Prostatic Prostatic

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DANIEL COHEN MARTN BLUMENFELD,IIVA CHUMAKOV,LUDIE BOOGELERET PC

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C12NS/50,C12NS/00,

CC C12NS/50,C12NS/10,C12NS/10,C12P21/08,C12Q1/68,GQ1N33/50 PC

PC C12NS/50,C12NS/100

CC QUARTNEL COMEN MARTN BLUMENFEED,IIVA CHUMAKOV,LUDIE BOOGELERET PC

C12NS/50,C12NS/100,C12NS/10,C12P21/08,C12Q1/68,GQ1N33/50 PC

C12NS/50,C12NS/100

CC C12NS/50,C12NS/100

CC QUARTNEL CANNOT BLUMENFEED,IIVA CHUMAKOV,LUDIE BOOGELERET PC

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Location/Qualifiers
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	GGGTCT 2100	041 TGCTGCCCAGCGTCGTGCTCCTGGGCACGGCGCCCACCTACGTGTTGGCCTGGC
	CTACC 2040       CTACC 2040	1981 GCCGCCGAGCTGAGAAGATGCTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCTACC
	TCGCT 1980	1921 CCGCCTGCTGGCCGCGACTGAGGCCCGGGAGGCGGGGGGGG
	ATTGG 1920       ATTGG 1920	1861 TGGGGGCGGAGGCTGGGAGCGGGTGGCGGGCGGGCCCGGGCCCGGGCGGTGATTGG
•	GCGGC 1860	1801 CGGCGCACGCAGCCCCGCACTCGCCTACCCCGGCCCCGGGCGGCGGCGGCCCATGCGG
	GGGAG 1800       GGGAG 1800	1741 GAGCATCCCTGAGCCATCGATCCGGGAGGGCCGCGGGTTCCCTTGCTTTGCCGCCGGGAG
	GGTGT 1740       GGTGT 1740	1681 TGCCGCGGAGCCCCCTGCCCCGGCAGGGGGATGTGGCGATGGGTGAGGGTCATGGGGTGT
	3CGCGTTGT 1680          3CGCGTTGT 1680	1621 CGTGTTATTGCCGCCGAGGTGGAACTATGGCAACGGGCGACCAATCAGAAGGCGC 
	AGAGA 1620       AGAGA 1620	1561 GCCCGCGCCACAGCAGGTAGCTGTACTGCAACTGTCGGGCCCAAACCAATCAAGAGA
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	CACCT 1500       CACCT 1500	1441 ACCCGGACCCTCCTCCGGCCAGCACCCACCTTCACCCAGTTCCGTCAGTCGCCACC
	GAGGC 1440       GAGGC 1440	1381 TCCAGCGACCCTTAAACCTGACCGCGCACGTCCGGCCCGAGGGAGCAGAACAAGAGG
	GCAGC 1380       GCAGC 1380	1321 TAATTGTGTGCATCCCGGCGCCCCAGGGGCTTGTGAGCAGCAGGTGCGGGTTCCAGG
	TGCTC 1320	1261 GCCCAGGTGCCTGCAAGAATTAGACCTCCGATAACGTTAACACCCCACTTTCTCACTGCTC   +
	CCTGG 1260       CCTGG 1260	1201 GTGAGCAGATGGGGACACTCGAGCTGCCCGCGGACCTGGGCCGAGCTGCCTACAAC
	TGGCA 1200       TGGCA 1200	1141 GGCTGCTGCGCACTCAGAGCGGAGGCTGAGGAGGCGGCGTCCCCTTGCAAAGGACTGG
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,			COMPLEX	KEYWORDS SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 2 BD196564 LOCUS DEFINITION ACCESSION	Qу 2: Дь 2:	Qy 2.	Db 2:
73 , 110 ,	CC upstream amplification primer 99-619, complement CC upstream amplification primer 4-76 CC downstream amplification primer 4-76, complement CC upstream amplification primer 4-77, complement CC upstream amplification primer 4-77, complement CC upstream amplification primer 4-71 complement CC upstream amplification primer 4-71 complement CC upstream amplification primer 4-72 complement CC downstream amplification primer 4-72 complement CC upstream amplification primer 4-72 complement CC	63 5-63 , complement 2 -622 , complement -621 , complement	PN JP 200251657-A/153  PN JP 200251657-A/153  PD 11-JUN-2002  PF 22-DEC-1998 JP 2000525562  PF 22-DEC-1997 US 08/996306.09-SEP-1998 US 60/099658 PI  DANIEL COHEN, MARTA BLUMENFELD, ILYA CHUMAKOV, LYDIE BOUGUELERET PC C12N15/09, C12N15/09, A01X67/027, C07X14/47, C07X16/18, C12N1/15, PC C12N1/19, PC C12N1/21, C12N5/10, C12N5/10, C12P21/08, C12Q1/68, G01N33/50 PC C12N15/00, C12N5/00, PC C12N15/00, C12N15/00  CC exon1  CC exon2	JP 2002516657-A/153.  JP 2002516657-A/153.  Homo sapiens (human)  Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 56520)  Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.  Prostatic cancer gene  Patent: JP 2002516657-A 153 11-JUN-2002;  GENSET  OS Homo saniens (human)	BD196564 Prostatic cancer gene. BD196564	281 GCTCCCCCACAGCTGGCGAGGGTCACCCGGCCGGCCGGCC	121   GCCGCCTCCCGGCTCCCGGGTCTCGGCGTCCACCCGAGCTCCCCGGGGGGGG	2101 GGCGGCTGCTCCCGCCTTCCTGCCCGCCCGCTTCTACCAAGCGCTGGACGACCGGCTGT 2160

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Query Match Query Match B6.1%; Score 2000; DB 6; Length 2000; Best Local Similarity 100.0%; Pred. No. 0; Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 GTGGATCTGTGGACTGTTCGCAGGAAGAGAGAGAGAGAGA	PF 22-DEC-1998 JP 2000525562  PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI  DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC C12N1/19, C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/00, PC C12N15/00,C12N5/00, PC C12N15/00,C12N5/00 CC Prostatic cancer gene FH Key Location/Qualifiers FT Source 1.2000 PT Location/Qualifiers 1.2000 FT Location/Qualifiers 1.2000 FT Location/Qualifiers 1.2000 forganism="Homo sapiens" /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	ACCESSION BD19565 ACCESSION BD195655.  WERSION BD195655.  GI:33006335  KEYWORDS JP 2002516657-A/154.  SOURCE Homo sapiens CRANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE AUTHORS Cohen, D., Blumenfeld, M., Chumakov, I. and Bougueleret, L.  PITILE Prostatic cancer gene JOURNAL Patent: JP 2002516657-A 154 11-JUN-2002; GENSET OS Homo sapiens (human) PN JP 2002516657-A/154 PD 11-JUN-2002	Qy 2161 ACTGCGTCTACCAGAGCATGGTGCTCTTCTTCGAGAATTACACCGGGGTCCAGGTGA 2220  Db 2161 ACTGCGTCTACCAGAGCATGGTGCTCTTCTTCTTCGAGAATTACACCGGGGTCCAGGTGA 2220  Qy 2221 GCCGCCTCCCGGCTCTCGGGTCTACCAGGGTCCACCGGGGTCCACCGGGGTCCACCGGGGTCCACCGGGGCCGGACCTCTCC 2280
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2 (Dases 1 to 165799)

2 (Dases 1, Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Birren,B., Linton,L., Nusbaum,C., Boguslavkiy,L., Boukhgalter,B., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitchugh,W., Gage,D., Galagan,J., Gardyna,S., Ferreira,P., Ford,S., Gord,S., Goyd,S., Goydette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
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AC100813.2 GI:22381986
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_CANCELLED.
Homo sapiens (human)
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacCorthy, M., Medrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Medrim, J., Weneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Scojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Con Aug 21, 2002 this sequence version replaced gi:17048183.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Web site: http://www-seq.wi.mit.edu
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2728 62827: gap of 100 bp

8828 73470: contig of 10643 bp in length

4471 73570: gap of 100 bp

1571 81515: contig of 7945 bp in length

1516 81615: gap of 100 bp

1616 165799: contig of 84184 bp in length.

Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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/clone_lib="CITD2 Human BAC"
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                                                                                              Rosenthal,A.
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REFERENCE
AUTHORS
Genome Sequencing Center Jena.
Direct Submission
Submitted (14-JUL-2000) Genome Au
Biotechnology, Beutenberstr. 11,
3 (bases 1 to 168136)
Reichwald, K. and Platzer, M.
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 168136)
Reichwald, K., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N., Reichwald, Y., Polley, A., Schilhabel, M.B., Taudien, S., Wen, G. and Renzel, U., Polley, A., Schilhabel, M.B., Taudien, S., Wen, G. and
                                                                                                                                     Chromosome 8 genomic sequence Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 (Dases 1 to 1007)
Lagemann, D. and Platzer, M.
Direct Submission
Submitted (03-APR-2002) Genome Analysis, Institute of Molecular
Submitted (03-APR-2002) Genome Analysis, Thuringia 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one pUC18 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biotechnology, Beutenberstr. 11, Jena, (Conses I to 168136)
Lagemann, D. and Platzer, M.
Direct Submission
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Submitted (29-MAR-2002) Genome Analysis, Institute or Motovern-
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4 (bases 1 to 168136)
Lagemann,D. and Platzer,M.
Direct Submission
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Submitted (23-AUG-2001) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neighboring sequence information:
This clone is overlapped by GS1-24F4, GS1-24F4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Quality Assessment:
                                                                                                                                                                                                                                                                Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                           This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H351
Center clone name: CTD-2541M15
Center clone name: CTD-2541M15
Center clone name: CTD-2541M15
Sequencing vector: pUC18; 100% of reads
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 16707 bases at least Q40
Consensus quality: 168133 bases at least Q30
Consensus quality: 168336 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://genome.imb-jena.de/
                                                                                                                                                                                                                       Location/Qualifiers
  organism="Homo sapiens"
|mol_type="genomic DNA"
                                                                   'map="p22-p21"
'clone="CTD-2541M15"
                                                                                                                                 organism="Homo sapiens"

(mol_type="genomic DNA"

(db_xref="taxon:9606"
                                                                                                                 chromosome="8"
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                    misc_feature
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95593..95693
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35987. .36115
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28243. .28507
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/clone="GS1-24F4"
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86073. .86097
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81070. .81071
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59027. .59136
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45312. .45406
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99495. .99715
                                                                                                                 /note="single stranded/single chemistry
98827. .98848
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78279. .78386
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OY 1138 AGGGGCTGCTGCGCACTCAGAGCCGAGGCTGAGGAGCGGCGTCCCCTTGCAAAGGACTG 1197	QY 1078 GTGATGGGGAAAAACACGGACCCTAATTCTGAAACACCCTGGTAGCGAGAGACGGGGAGG 1137	Qy 1018 GAAATATCCTTGTGGGATTGTTCTTCAGCTATGCATAAACATGTAATTATCATTACT 1077	Oy 958 CAACAGACTCTGAGGAAATGAAGCAAGAGTGAATTCTGAAAAGGTCTAATAAACAGTATG 1017	Qy 898 TACTTTAATTACTACAGAAAAAAACGAGGCTCCTTATTAAAAAAAA	Qy 838 GTAGCTTTTAGTGAAGGCTACAAAAGTATGCTTTTTATGGATTACACATGTGCACGCAAC 897	Qy 778 GAAAGATCCAAAAGTCCTGTGGATCTGCTTTAACATCAATAAAACAGTTATCCACCCTTC 837	Qy 718 ACAACTATCCTTGAAAAGGGTTACATATTAAACCATTTTTACCACAGCCAAAGGGGAGGA 777	ATATATATATATATATATATATGGTAAAGCATTCGGCATTCTTTAAAGT 717 	Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	sc_feature /	feature	sc_feature 1	sc_feature	80   1 80   1	sc_feature sc_feature	sc_feature	chemistry
Q B Q			O B &	•					Qy Db	Qy dd	Db Qy	Ωy	dd Qy	QQ	D Q	Qy Db	da
2218 TGAGCCGCTCCCGCTCCCCGGTCTCCGCGCTCCCAACTCCCGAGCTCCCGAGCTCCCGAGCTCCCGAGCTCCCGAGCTCCCGAGCTCCCGAGCTCCCGAGCTCCCGAGCTCCCCGAGCTCCCCGGGGCGGACCTC 114441 114382 TGAGCCGCCTCCCGGCTCCCGGGCTCCACCCGAGCTCCCCGGGGGGGCGGACCTC 114441 2278 TCCGCTCCCCCACAGCTGGCGAGGGTCACCCGGCCGGCCG	322 TCTACTGCGTCTACCAGAGCATGGTGCTCTTCTTCGAGAATTACACCGGGGTCCAGG		2098 TCTGCTGCTCTCCGCCTTCCTGCCGCCTGCCGCTTCTACCAAGCGCTGGACCGGC 2157	1978 GCTGCCGCCGAGCTGAGAAGATGCTGCTGCTCCCTGGTGCTCCCACACGTACTCCATGCGCT 2037	1918 TGGCCGCCTGCTGGCCGCGACTGAGGCCCGGGAGGCGGGGGGGG	1858 GGCTGGGGGCGCAGCTGGGAGCCGGTGGCCGGGCCCCGGGCCCCGGCCCTGAT 1917	1798 GARCIGGCACGAGCCCCGCACTCGCCTACCCCGGGCGCGGCGGCGGCGGCGGCGCCCATGC 1857	738 TGTGAGCATCCCTGAGCCATCGATCCGGGAGGGCCGGGTTCCCTTGCTTG	1678 TGTTGCCGCGGAGCCCCTGCCCCGGCAGGGGATGTGGCGATGGGTGAGGGTCATGGGG 1737	1618 AGACGTGTTATTGCCGCCGAGGTGGAACTATGGCAACGGGCGACCAATCAGAAGGCGCGT 1677	1558 GTTGCCCGCGCCACAGCAGGTAGCTGTACTGCAACTGTCGGCCCAAACCAACC	1498 CCTCCCTTCCCGCGCTCCGCAGCCGGCCCAGCTGGGGAAGCATGCGCAGTGGCCGGAGCCGG 1557	1438 GGCACCCGGACCCTCCTCCGGCCAGCACCCACCTTCACCCAGTTCCGTCAGTCGCCACCA 1497	1378 AGCTCCAGCGACCCTTAAACCTGACCGCGCGCACGTCCGGCCCGAGGGAGCAGAACAAGA 1437 	1318 CTCTAATTGTGTGCATCCCGGCGCCCAGGGGCTTGTGAGCAGCAGCTGCGCGCTTCCAGGC 1377	1258 TGGGCCCAGGTGCCTGCAAGAATTAGACCTCCGATTAACACCCACTTTCTCACTG 1317	362

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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meddrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2001 this sequence version replaced gi:12313816. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183485)
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Homo sapiens clone RP11-15C20, WORKING
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                                                                                                                                                                                                                           web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center clone name: 15.C_20
Center clone name: 15.C_20
Center clone name: 15.C_20
Sequencing vector: M13, M77815; 4% of reads
Sequencing vector: M13, M77815; 96% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0,960731
Consensus quality: 179658 bases at least Q30
Consensus quality: 181356 bases at least Q30
Consensus quality: 182011 bases at least Q30
Insert size: 170000; agarose-fp
Insert size: 182485; sun-of-contigs
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                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                        Quality coverage: 7.0 in Q20 bases; agarose-fp Quality coverage: 6.5 in Q20 bas.

NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                           as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://v
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1387: contig of 1387 bp in length
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                                                                 GCTACAAAAGTATGCTTTTTATGGATTACACATGTGCACGCAACTACTTTAATTACTACA 913
                                                                                                                                                                                              AGGGTTACATATTAAACCATTTTTACCACAGCCAAAGGGGGAGGAAAGATCCAAAAGTC
                                                                                                                                                                                                                             AGGGTTACATATTAAACCATTTTTACCACAGCCAAAGGGGAGGAGGAAGATCCAAAAGTC 793
                                                                                                                                                                                                                                                                                                             ATATATATATATATATGGTAAAGCATTCGGCATTCTTTTAAAGTACAACTATCCTTGAAA
                                                                                                                                   CTGTGGATCTGCTTTAACATCAATAAAACAGTTATCCACCCTTCGTAGCTTTTTAGTGAAG 853
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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126278: contig of 59121 bp
126378: gap of 100 bp
183485: contig of 57107 bp
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g of 59121 bp
f 100 bp
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g of 17868 bp :
f 100 bp
g of 23182 bp :
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COMMENT

	T 2053	1994 GAAGATGCTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCTACCTGCTGCCCAGCG	
	A 1993   A 74252	1934 GCGACTGAGGCCCGGGAGGCGGGGGGGGGGGGGGGGGGG	
1	C 1933   C 74192	1874 TGGGAGCGGGTGGCGGGCGGGCGGGCCCGGGCCCGGGCGGTGATTGGCCGCCTGCTGGC	
	C 1873   C 74132	1814 CCCGCACTCGCCTACCCGGCCCCGGGCGGGGGGGGGGGG	
	C 1813   C 74072	1754 CCATCGATCCGGGAGGGCCGCGGGTTCCCTTGCTTTGCCGCCGGGAGCGGGGCGCACGCA	
	G 1753   G 74012	1694 CCTGCCCCGGCAGGGGGATGTGGCGATGGGTTGAGGGTCATGGGGTGTGAGCATCCCTGAG	
	C 1693   C 73952	1634 CCGAGGTGGAACTATGGCAACGGGCGACCAATCAGAAGGCGCGTTGTTGCCGCGGAGCCC	
	G 1633   G 73892	1574 CAGGTAGCTGTACTGCAACTGTCGGCCCAAACCAATCAAGAGACGTGTTATTGCCG	
	G 1573   G 73832	1514 CGCAGCCGGCCCAGCTGGGGAGCATGCGCAGTGGCCGGAGCCGGGTTGCCCGCGCCACAG	
	C 1513	1454 TCCGGCCAGCACCCACCTTCACCCAGTTCCGTCAGTCGCCACCACCACCTCCCTTCCCGCGT	
<del></del>	C 1453   C 73712	1394 AAACCTGACCGCGCGCGCACGTCCGGCCCGAGGGAGCAGAACAAGAGGCACCCCGGACCCTC	
	r 1393   r 73652	1334 CCCGGCGCCCAGGGGCTTGTGAGCAGCAGGTGCGCGTTCCAGGCAGCTCCAGCGACCCTT	
	r 1333 r 73592	1274 CAAGAATTAGACCTCCGATAACGTTAACACCCACTTTCTCACTGCTCTAATTGTGTGGAT 	
	3 1273   3 73532	1214 GACACTCGAGCTGCCCCGCGACCTGGGCCGAGCTGCCTACAACCTGGGCCCAGGTGCCTG	
	3 1213   3 73472	1154 TCAGAGCGGAGGCTGAGGAGGCGGCGTCCCCTTGCAAAGGACTGGCAGTGAGCAGATGGG	
	1153 73412	1094 CGGACCCTAATTCTGAAACACCCTGGTAGCGAGAGACGGGCAGGAGGGGGCTGCTGCGCAC	
	1 1093 1 1 73352	1034 ATTGTTCTTCAGCTATGCATAAACATGTAATTATCATCATTACTGTGATGGGGAAAAACA	
	3 1033 3 73292	974 AATGAAGCAAGAGTGAATTCTGAAAAGGTCTAATAAACAGTATGGAAATATCCTTGTGGG 	
·	973 173232	914 GAAAAAAACGAGGCTCCTTATTAAAAAAAATCAGAAACAAGTCCAACAGACTCTGAGGA 	

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RESULT 7 ACC091099 LOCUS DEFINITION ACCESSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS AUTHORS AUTHORS AUTHORS REFERENCE AUTHORS	Db 74253 Qy 2054 Db 74313 Qy 2114 Db 74373 Qy 2174 Db 74433 Qy 2234 Db 74493 Db 74493 Db 74553
100 ACO91099 ACO91099 CO9718 bp DNA linear HTG O6-AUG-2002 BOWN Homo sapiens chromosome 8 clone RP11-782N1 map 8, WORKING DRAFT SEQUENCE, 10 unordered pieces.  RC091099.3 GI:22122960 ACO91099.3 PROBLEM FOR SEPTION FOR ACO91099.3 GI:22122960 ACO91099.3 GI:22122960 ACO91099.3 GI:22122960 ACO91099.3 FROM FOR ACO91099.3 PROBLEM FOR ACOME ACOM	

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FEATURES
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                                                                                                                                                                                  source
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Sequencing vector: Plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 206663 bases at least Q40 Consensus quality: 207712 bases at least Q20 Consensus quality: 207712 bases at least Q20 Consensus quality: 208309 bases at least Q20 Insert size: 205000; agarose-fp Insert size: 205000; agarose-fp Quality coverage: 8.8 in Q20 bases; agarose-fp Quality coverage: 8.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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----- Project Information
Center project name: L12159
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                                            /mol_type="genomic un
/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                               organism="Homo sapiens"
clone="RP11-782N1"
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    Genome Center

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                                                                                          CTGTGGATCTGCTTTAACATCAATAAAACAGTTATCCACCCTTCGTAGCTTTTTAGTGAAG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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CTGGGAGCGGGTGGCGGCCGGCCCGGGCCCGGGCCGGGTGATTGGCCGCCTGCTGGC 1932
CCCCGCACTCGCCTACCCGGGCCCGGGCGGCGGCGCGCCCATGCGGCTGGGGGCGGAGG 1872
3CGGCGCACGC-AG 1812            3CGGCGCACGCAAG 103853
CTGCCCCGGCAGGGGGATGTGGCGATGGGTGAGGGTCATGGGGTGTGAGCATCCCTGAG 1753 
CGAGGTGGAACTATGGCAACGGGCGACCAATCAGAAGGCGCGTTGTTGCCGCGGAGCCC 1693 
CAGGTAGCTGTACTGCAACTGTCGGCCCAAACCAACCAATCAAGAGACGTGTTATTGCCG 1633
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CAAGAATTAGACCICCGATAACGITAACACCCACTTTCICACTGCTCTAATTGIGTGCAT 1333 
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CTATGCATAAACATGTAATTATCATCATTACTGTGATGGGGAAAAACA 1093 
AATGAAGCAAGAGTGAATTCTGAAAAGGTCTAATAAACAGTATGGAAATATCCTTGTGGG 1033 
GAAAAAACGAGGCTCCTTATTAAAAAAAAATCAGAAACAAGTCCAACAGACTCTGAGGA 973 
GCTACAAAAGTATGCTTTTTATGGATTACACATGTGCACGCAACTACTTTAATTACTACA 104753

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Sequence 2 from Patent W00134782.
AX141275
                                                                                                                                                                                                                                                                                                                                                              Human lysophosphatidic acid acyltransferase_g(e)
Patent: WO 0134782-A 2 17-MAY-2001;
CELL THERAPEUTICS, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
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/db_xref="taxon:9606"
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             1793 GCCGGGAGCGCACGCAGCCCCGCACTCGCCTACCCGGCCCCGGGCGGCGGCGCGCCC 1852
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Homo sapiens lysophosphatidic acid acyltransferase-epsilon
(LDAAT-e) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-MAY-2001) Mol. Elliott Ave., W., Suite 400, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1509)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning and expression Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF375789.1 GI:14161584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leung, D.W
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                                                                                                                                              Similarity
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                                                                                      TGGGGTGTGAGCATCCCTGAGCCATCGATCCGGGAGGGCCGCGGGTTCCCCTTGCCTTTGCC 1792
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                                                                                                                            Conservative
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                                                                                                                                                                                                                 /product="1y8ophosphatidic acid acyltransferase-epsilon"
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DIAIRQNALGHVRYYLKEGLKWLPLYGCYFAQHGGIVYKRSAKFNIKEMRNKLQSYV
DAGTPMYLVIFPEGTKYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATHYCDCM
KNYLDAIYDVTVYYEGKDDGGQRRESPTWTEFLCKECPKIHHIDRIDKIDKKDVPEEQEH
MRRWLHERFEIKDKMLIEFYESDDPERRKRFPGKSVNSKLSIKKTLPSMLILSGLTAG
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/EC_number="2.3
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...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                              note="1-acylglycerol-3-phosphate O-acyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          map="8pter-p23.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      number="2.3.1.51"
                                                                                                                                            18.6%;
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                                                                                                                      Score 433; DB 9; 1
Pred. No. 4.3e-235;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell Therapeutics, Inc.,
e, WA 98119, USA
                                                                                                                                                         Length 1509;
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AUTHORS
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                                                                                                                                                                               TITLE
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                                                                                                                                                                     Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuk, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dikson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC023550 1503 bp mRNA
Homo sapiens acid acyltransferase-epsilon,
MGC:15506 IMAGB:4129973), complete cds.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                   Strausberg, R.
                                                                                                                                          Proc. Natl.
                                                                                                                                            human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
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PRI 06-OCT-2003

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Best Local Similarity
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                                                                                                                                                                                   1742 AGCATCCCTGAGCCATCGATCCGGGAGGGCCGCGCGGTTCCCTTGCTTTGCCGCCGGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G. Breen,K., Brinkley,C., Brooks,S.,
Blatch,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 27 Row: m Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8922941.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Aug 19, 2003 this sequence
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaithersburg, Maryland;
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    AGCATCCCTGAGCCATCGATCCGGGAGGGCCGCGGGTTCCCTTGCCTTTGCCGCCGGGAGC
                                                                                                                                                                                                                                   Conservative
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257. .1351
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/clone="MGC:19506 IMAGE:4129973"
                                                                                                                                                                                                                                                                                                                                                 /note="PlsC; Region: Phosphate acyltransferases"
/db_xref="CDD:smart00563"
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this sequence version replaced
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                                                                                                                                                                                                                                                        Score 424; DB 9;
Pred. No. 6e-230;
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AX268078
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Williamson,M.
46743 and 27417, novel human acyltransferase family members and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="01:16516594"
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RFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDLEKNKENIIYLANEKSTWUWIVA-
RFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDLEKNKENIIYLANGSTVUWSKRENIKKATHVAFDCM-
DILALRQNALGHVRYVILKEGLEKNLFLYGCYFAQHGGIVVKRSAKENEKEMRUKLOGYV-
DAGTPMYLVI FPEGTRYNEGQTKVLSASQAFFAAQRGLAVLKHVLTPRIKKGTHVAFDCM-
KNYLDAIYDVTVVYEGGNDGGQRRESFTMTEFICKECTKIHHIDRIDKXDVPEEQEH-
MRRWILBRIGHTSTENGKMLIEFYESPDPERRKRFFGKSVNSKLSIKKTLPSMLILSGLTAG-
MRRWILBRIGHTSTENGKMLIEFYESPDPERRKRFFGKSVNSKLSIKKTLPSMLILSGLTAG-
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                  OS Homo sapiens (human)

PN JP 2002516657-A/104

PD 11-JUN-2002

PF 22-DEC-1998 JP 2000525562

PF 22-DEC-1999 US 2009525562

PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI

DANIEL COHEN, MARTA BLUMENFELD, ILYA CHUMAKOV, LYDIE BOUGUELERET PC

C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC

C12N1/19,
                                                                                                           Cohen, D., Blumenfeld, M., Chumakov, I. and Bougueleret, L. Prostatic cancer gene Patent: JP 2002516657-A 104 11-JUN-2002; GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BD196515
BD196515.1 GI:33006285
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Prostatic cancer gene.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                             misc_feature 31. .33
misc_feature 235. .237
polyA_signal 4531. .4536.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                     .4558
 9.3%;
Score 217; DB 6; Li
Pred. No. 1.1e-111;
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KEYWORDS
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BD196497
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DEFINITION
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Best Local Similarity
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PN JP 2002516657-A/86
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PF 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN, MARTA BLUMENHFELD, ILYA CHUMAKOV, LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216)
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PC C12N5/00,C12N15/00
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JP 2002516657-A/86.
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BD196497
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                   CTGCCCGCCCGCTTCTACCAAGCGCTGGACGACCGGCTGTACTGCGTCTACCAGAGCATG
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                                                                                                                                                                                                                                                                                                                             /organism='Homo sapiens
                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                      9.3%;
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                                                                                                                                                                                     Score 216; DB 6; ; Pred. No. 3e-111; 0; Mismatches 0
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1. .216
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180
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SOURCE
ORGANISM
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BD196514
LOCUS
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Search completed: May 26, 2004, 10:29:32 
Job time : 8839.79 secs
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PN JP 2002516657-A/103

PD 11-JUN-2002

PF 22-DEC-1998 JP 2000525562

PF 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI

DANIEL COCHEM, MARTA BLUMENFELD, ILYA CHUMAKOV, LYDIE BOUGUSLERET PC

C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC

C12N11/19,

PC C12N15/00,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC

CC12N15/00,C12N5/00,

PC C12N5/00,C12N5/00,

PC C12N5/00,C12N5/00,

PC C12N5/00,C12N5/00,

PC G12N5/00,C12N5/00,

PC G12N5/00,C12N5/00,

PC G12N5/00,C12N5/00,

PC G12N5/00,C12N5/00

CC ANTAAA

FH Key

FT misc_feature 31. 33

FT misc_feature 31. 33

FT misc_feature 31. 303

FT polyA_signal 4655. 46660.
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                                                                                 181 GTGCTCTTCTTCGAGAATTACACCGGGGTCCAG 216
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4682)

1 (Chen, D., Blumenfeld, M., Chumakov, T. and Bougueleret, L.

Prostatic cancer gene
Patent: JP 2002516657-A 103 11-JUN-2002;

GENSET

OS Homo sapiens (human)
PN JP 2002516657-A/103
PD 11-JUN-2002
PF 22-DEC-1998 JP 200525562
PF 22-DEC-1997 US 08/993306,09-SEP-1998 US 60/099658 PI
PR 22-DEC-1997 US 08/993306,09-SEP-1998 US 60/099658 PI
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JP 2002516657-A/103.
Homo sapiens (human)
Homo sapiens
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polyA_signal 4655. ..
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                Score
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## ALIGNMENTS

	LOCUS	BX332287 1201 bp mRNA linear EST 02-MAY-2003
	DEFINITION	Homo sapiens NEUROBLASTOMA COT 25-
		cDNA clone CS0DC010YJ07 5-PRIME, mRNA sequence.
	ACCESSION	BX332287
	VERSION	BX332287.1 GI:30337119
	KEYWORDS	EST.
	SOURCE	Homo sapiens (human)
	ORGANISM	Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	REFERENCE	1 (bases 1 to 1201)
	AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
to have a	TITLE	Full-length cDNA libraries and normalization
being printed,	JOURNAL	Unpublished (2001)
ion.	COMMENT	Contact: Genoscope
		Genoscope - Centre National de Sequencage
		BP 191 91006 EVRY cedex - France
		Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
		Library was constructed by Life Technologies, a division of
scription		Invitrogen. This sequence belongs to sequence cluster 5026.f For
		more information about this cluster, see
1197695 602757619		cai-bin/cluster.cai?sea=CSODC010CE04OP1&cluster=5026.f. Contact :
560635 AL560635		Feng Liang Email : fliang@lifetech.com URL :
I913991 603180569		http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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RESULT 2
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 822)
1 (bases 1 to 822)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Faraday Avenue Genoscope sequence ID : CSODCO10CE04QP1.
Location/Qualifiers
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602757619F1 NIH_MGC_19 Homo
                                                                                                                   Homo sapiens (human)
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                                                                                                                                                                           mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODCO10YJ07"
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Pred. No. 2.6e-207;
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EST.
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Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1774 row: f column: 05
High quality sequence stop: 753.
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/clone lib="NH108 (phage-resistant)"
/clone lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2
BcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                        Homo
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/db_xref="taxon:9606"
/clone="IMAGE:4892932"
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|mol_type="mRNA"
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                                                               1005 bp mRNA linear EST 31-MAY-2003 o sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED CDNA clone CSODL003YD01 5-PRIME, mRNA sequence.
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Pred. No. 1.7e-189;
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1 (bases 1 to 1005)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12907288.

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIo3CB01QP1&cluster=5026.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODIo03CB01QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5026.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                      CGCCTCCCGCTCCCGGGTCTCGGCGTCCACCCGAGCTCCCGGGGGGCGCGGACCTCTCCGC 2282
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Carity 99.4%;
Conservative
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/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_line="RAMOS CELL LINE"
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'db_xref="taxon:9606"
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Pred. No. 6.4e-166;
D; Mismatches 3;
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2230 CGCTCCCGGGTCTCGGCGTCCACCCGAGCTCCCGGGGGGCGCGGACCTCTCCGCTCCCCCA 2289
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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(bases 1 to 787)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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Location/Qualifiers
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.7-3.5 kb. Library is norm full-length clones and was (Invitrogen). Research Gene this is a NIH_MGC Library."
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|mol_type="mRNA"
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'clone="IMAGE:5244761"
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100.0%; Pr
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Pred. No. 1.5e-149;
0; Mismatches 0;
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                                                                                                                                                        61
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High quality sequence stop: 517.
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
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602866369F1 NIH_MGC_7 Homo
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI116158
BI116158.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                                                                                           GCGATGGGTGAGGGTCATGGGGTGTGAGCATCCCTGAGCCATCGATCCGGGAGGGCCCGCG 1775
                                              GCGGCCCGGGCCCGGGATTGGCCGCCTGCTGGCCGACTGAGGCCCGGGAGGCC
                                                                                                       CGGGCGGCGGCGGCCCATGCGGCTGGGGGCGGAGGCTGGGAGCGGGTGGC-GGGCGCG
                                                                                                                                                      GGTTCCCTTGCTTTGCCGCCGGGAGCGGCACGCAGCCCCGCACTCGCCTACCCGGCCC
                                                                                                                                                                                                                          GCGATGGGTGAGGGTCATGGGGTGTGAGCATCCCTGAGCCATCGATCCGGGAGGGCCGCG
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                                                                                    CGGGCGGCGCCCATGCGGCTGGGGGCGGAGGCTGGGAGCGGGTGGCTGGGCGCG
                 GCGGCCCGGGCCCGGTGATTGGCCGCCTGCTGGCCGCGACTGAGGCCCGGGAGGCG
                                                                                                                                                                                                                                                                                                                                                     /cell lTne="MGC3"
/lab host="DH10B (phage-resistant)"
/clome_lib="NHH MGC_7"
/clome_lib="NHH MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: Mote="Organ: lung; Vector: poTB7; Site_1: XhoI; Site_2: Cloned into EccRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZMP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/db_xref="taxon:9606"
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Pred. No. 3.8e-147;
0; Mismatches 1;
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10 sapiens cDNA clone
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one IMAGE:5015128 5',
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Matches 411
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                1747 CCCTGAGCCATCGATCCGGGAGGGCCGCGGGTTCCCTTGCTTTGCCGCCGGGAGCGGCGC 1806
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602752872F1 NIH_MGC_17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 717)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, N
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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                                                                Similarity
                                                  Conservative
                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4905832"
                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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                                                              12.5%;
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                                              Score 291; DB 12;
Pred. No. 2.3e-128;
0; Mismatches 0;
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1955 GGCGGGGAGCGCAGGCGGAGCTCGCTGCCGCCGAGCTGAGAAGATGCTGCTGTCCCTGGT 2014
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCML807 row: o column: 17
High quality sequence stop: 681.
Location/Qualifiers
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                                                                                        /note="Organ: muscle; Vector: pOTB7; Site_1: ECORI; Site_2: XhOI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information (
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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primer: M13 Forward.
                                                                                                                                     /organism="Homo sapiens"
/mol_type="maNA"
/db xref="taxon:9606"
/clone="IMAGB:3066752"
/tissue_type="lymph"
/cell_type="germinal center B 
Location/Qualifiers
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Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 3528
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: John Quackenbush
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  ACAACTATCCTTGAAAAGGGTTACATATTAAACCATTTTTACCACAGCCAAAGGGGAGGA
                                                                          ATATATATATATATATATATATATATATATATGGTAAAGCATTCGGCATTCTTTTAAAGT
                                                                                                  ATATATATATATATATATATATATATATATATGGTAAAGCATTCGGCATTCTTTAAAGT 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         johnq@tigr.org
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                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone_lib="MAGE resequences,
/note="Vector: pBluescriptSKm"
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                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"

mol_type="mRNA"
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0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5026.f
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Faraday Avenue Genoscope sequence
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgi-bin/cluster.cgi?seq=CSODA011BD07QP1&cluster=5026.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.genoscope.cns.fr/
                                                                                                                                                                  Similarity
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                                                               GCGCACGCAGCCCCGCACTCCGCCTACCCCGGCCCCGGGCGGCGGCGGCCGATGCGGCTG
                                                                                                       GCGCACGCAGCCCCGCACTCGCCTACCCGGCCCCGGGCGGCGGCGCGCCCCATGCGGCTG
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                                                                                                                                             Conservative
                                                                                                                                                                                                                                            /tissue_type="NEUROBLASTOMA" /clone_Tib="Homo sapiens NEUROBLASTOMA" /clone_Tib="Homo sapiens NEUROBLASTOMA" /note="Vector: pc/NySpORT_6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned ithe Not I and EcoRV sites of the pcMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA011YG14"
                                                                                                                                                              11.2%;
99.3%;
                                                                                                                                             0
                                                                                                                                           Score 261; DB 9;
Pred. No. 6.1e-114;
0; Mismatches 3;
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340 bp mRNA linear EST 03-OCT-20
TCBAP2E4537 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4537, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: clones@txccc.org
Citation: Carninci,P. and Hayashizaki,Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalia; Eutheria; Primates; Catarrhini; Hominic 1 (bases 1 to 340)
wei, Y., Tsang, Y. T.M., Mei, G., Ku, J.M., Ali-Osman Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F. Pediatric Leukemia cDNA Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at Baylor College of Medicine
1102 Bates, MC3-3320 Houston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas Children's Cancer Center and Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                          leukemīa Baylor-HGSC project=TCBA"

/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
/rist strand cDNA was primed with an anchored

XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGCGCAGGAG(T)VN

XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGCCCCAGGAG(T)VN

3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
was primed with a BamHI-dC primer

[5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3'].
                 Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of
                                                                                                                                                                                                                                     /tissue_type="leukopheresis"
/cell_type="pre-B_cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 clone="TCBAP4537"
                                                                                                                                                                                                                                                                                                                          sex="male"
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  and
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BX473402
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                                                                                                                                                                                                                                    Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S. EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX473402
BX473402.1 GI:31667652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX473402 567 bp mRNA linear DKFZp686F16162_r1 686 (synonym: hlcc3) Homo sapiens DKFZp686F16162_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  This clone (DKF2p686F16162) is available at the RZPD in Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
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/mol type="maNA"
/db xref="taxon:9806"
/clone="DKFZp686F18162"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="d86 (synonym: h
/note="Vector: pTriplEx2; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
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hlcc3)"
Site_1: SfiIA;
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REFERENCE
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BU154303
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ORGANISM
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Matches 227
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Best Local Similarity
Matches 227; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 892)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
Unpublished (1999)
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AGENCOURT_7832759 NIH_MGC_
                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bloscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13469 row: j column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5', mRNA sequence.
BU154303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU154303.1
                                                                                   Similarity
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                                  GTCATGGGGTGTGAGCATCCCTGAGCCATCGATCCGGGAGGGCCGCGGGTTCCCCTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTCCGCCTTCCTGCCCGCCCGCTTCTACCAAGCGCTGGACGACCGGCTGTACTGCGTCT 2169
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                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 242.
Location/Qualifiers
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens (human)
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                                                                                                                                                     /tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clome lib="NIH MGC 67"
/note="Torgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
Technologies."
                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6144491"
                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:22667835
                                                                                   9.8%;
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                                                                                   Score 227; DB 13; Pred. No. 1.4e-97;
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Pred. No. 1.5e-97;
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  Best Local Similarity Matches 223; Conserv
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1 (bases 1 to 687)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R. Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM789163 6
K-EST0068703 S11SNU1 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 687.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: yongsung@mail.kribb.re.kr
Plate: 25 row: E column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21C Frontier Korean EST Project 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +82-42-860-4409
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9.6%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                /note=Torgan: Stomach; Vector: pME18-FL3; Site 1: XhoI;
/note=Torgan: Stomach; Vector: pME18-FL3; Site 1: XhoI;
/site 2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including Sfil
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript I using Sfil
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaCH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with Sfil and
cloned into DraIII digested pME188-FL3 vector. The
                                                                                                     obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphoblast-like"
/cell_line="SNU-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="Stomach"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="S11SNU1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="S11SNU1-25-E07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (2002)
  Score 223; DB 12;
; Pred. No. 1.2e-95;
0; Mismatches 0;
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                                         DB 12; Length 687;
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  Indels
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Kim,S. and
  Gaps
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                                                                                                                             Best Loc
Matches
                                                                                                                                                                       Query Match
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Local

Similarity

9.5%; Score 221; DB 13; 100.0%; Pred. No. 1.1e-94; tive 0; Mismatches 0;

Length 1216; Indels

0

Gaps

0

Conservative

1799

1739 GTGAGCATCCCTGAGCCATCGATCCGGGAGGGCCGCGGGTTCCCTTGCCTTTGCCGCCGGG

34 GTGAGCATCCCTGAGCCATCGATCCGGGAGGGCCGCGGGTTCCCTTGCTTTGCCGCCGGG

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REFERENCE
AUTHORS
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VERSION
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BU931112
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ORIGIN
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ORGANISM
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AGENCOURT 10475891 NIH MGC 109 Homo
IMAGE: 6671220 5', mRNA sequence.
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High quality sequence stop: 269.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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                                          /clone="IMAGE:6671220"
/tissue_type="teratocarcinoma, cell line"
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/clone_lib="NIH1MGC_109"
/clone_fib="NIH1MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2: MnOI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubbin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                      NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:9606"
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Qy         2000 GCTGCTGTCCC                                 Db         2 GCTGCTGTCCC           Qy         2060 CCTGGGCACGC                                 Db         62 CCTGGCCACGC           Qy         2120 CCTGCCCGCC           Qy         2120 CCTGCCCGCC           Qy         122 CCTGCCCGCCC	y Match Local Siπ hes 217;	Ingolstaedter This is the 5 Clone from S. Sequenced by I Heidelberg/Ge: German Genome No s1 sequency This clone (D) Please contact Berlin-Charlot FEATURES Source 1(b) //cloi//	Mewes,H.W., Weil,B., Wiemann,S. TITLE EST (Poustka,A., Albe Wellenreuther,R., et JOURNAL Unpublished (2003) COMMENT Contact: MIPS MIPS	VERSION BX5074091 C KEYWORDS EST. SOURCE Homo sapiens ORGANISM Homo sapiens Eukaryota; Me Mammalia; Eut REFERENCE 1 (bases 1 t) AUTHORS Poustka, A., I	LT 15 7409 8 BX507409 NITION DKFZp7790084 DKFZp7790084	Qy 1919 GGCCGCCTGCT	Qy 1859 GCTGGGGGCGC           Db 154 GCTGGGGGCGC	Db 94 AGCGGCGCACC
GCTGCTGTCCCTGGTGCTCCACACGTACTCCATGCGCTACCTGCTGCCCAGCGTCGTGCT 2059	9.3%; Score 217; DB 13; Length 643; ilarity 100.0%; Pred. No. 9.4e-93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Ingolstaedter Landstr.1, D-85764 Newherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available. No sl sequence available. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers 1.643 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="DKFZD7790084" /tissue_type="minna" /tissue_type="liver" /lab_host="DH108" /clone_lib="779 (synonym: hnccl)" /note="Vector: pSportl_Sfi; Site_1: SfiIA; Site_2: SfiIB"	Amid,C., Osanger,A., Fobo,G., Han,M. and rt,R., Moosmayer,P., Schupp,I., al.)	.:32051430 (human) (human) (azoa; Chordata; Craniata; Vertebrata; Euteleleria; Primates; Catarrhini; Hominidae; Homo.) (43) (bert,R., Moosmayer,P., Schupp,I., Wellenreut	643 bp mRNA linear EST 04-SEP-2003 _r1 779 (synonym: hncc1) Homo sapiens cDNA clone _5', mRNA sequence.	GGCCGCCTGCTGGCCGCGACTGAGGCCCGGGAGGCGGGCG	GCTGGGGGGGAGGCTGGGAGCGGGTGGCGGGCGCGGGCCCGGGCCCGGGCCGGGTGATT 1918	

182	2180
182 GGTGCTTCTTCGAGAATTACACCGGGGTCCAG 218	2180 GGTGCTCTTCTTCGAGAATTACACCGGGGTCCAG 2216

Search completed: May 26, 2004, 12:51:02 Job time: 5471.68 secs

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
sterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 209)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lai,C., Church,S., Jackson,L. and Bradford,K.
Letuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                      BQ989814
QGF18L11.yg.ab1 QG_EFGHJ
QGF18L11, mRNA sequence.
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
                                                                                                                                                                                                                                                                                                              http://compgenomics.ucdavis.edu/
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BQ989814.1 GI:22409349
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AL213828 Tetraodon
AV334716 AV334716
AZ726944 RPCI-24-1
BQ597016 PFESTOAD2
AI431315 ar55b9 x
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BH450006 BOHGB16TF
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AG144022 Pan trog1
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BZ508298 BONHJ80TF
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AK013575 Mus muscu
AV254417 AV254417
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BX721433 BX721433
BZ845349 CH240_250
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BG521596 NISC n111
M52378 zc48c05.s1
BH930122 odi98a04
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AV665533 AV665533
BU011575 QGJ16J71.
AV665534 AV665534
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EST 21-AUG-2002

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RESULT 2
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Plate: QGF18
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
spermatophyta; Magnollophyta; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                     Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                   http://compgenomics.ucdavis.edu/
Unpublished (2002)
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                                                                                                                                     Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cichorieae; Lactuca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 210)
                                                                                             details.
:e: QGA3 row:
                                                                                                                                                                                        1-(530)-742-1742
1-(530)-752-9659
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TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=GTTGCACGGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
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/mol_type="mRNA"
/cultivar="L.serriola"
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                      organism="Lactuca sativa"/
                                                                  Location/Qualifiers
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'clone="QGF18L11"
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_type="mRNA"
                                                                                             column: 09
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; Pred. No. 24;
0; Mismatches
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KEYWORDS
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BQ857992
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DEFINITION
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(bases 1 to 210)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Kin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elilison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops. R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGB9A22.yg.abl QG_ABCDI lettuce
QGB9A22. mRNA .....
                                                                                                                                                                                                                                                                                                                                                                                                                                      Asmundson Hall, UCD, 1
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://compgenomics.ucdavis.edu/
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                  Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig7771, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactuca sativa
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23; Conservative
                                                                                                                                                                                                                                                                                                                                details.
te: QGB9 row: A
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/note="Vector: pBRcDNASfiAB; The library was constructed
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_TISSUB=roots
TAG_TIB=OG_ABCDI lettuce salinas
/clome_lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each
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/clone="QGA3g09"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                     /db_xref="taxon:4236"
/clone="QGB9A22"
                                                                                                                                                                                                                            organism="Lactuca sativa"
|
| mol_type="mRNA"
                                                                                                                              'lab_host="E.coli"
                                                                                                                                                                                                          cultivar="Salinas"
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100.0%; Pr
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24;
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BQ992394
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ORIGIN
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Best Local Similarity
Matches 23; Conserv
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1 (bases 1 to 222)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGP25103.yg.abl QG EFGHJ lettuce serriola Lactuca sativa cDNA clone QGF25103, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
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Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           details.
te: QGF25
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                                                                                                                    Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library
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                       TAG_TISSUE=roots
TAG_LIB=QG_EFGHJ_lettuce_serriola
TAG_SEQ=GTTGCACGGG"
                                                                                               construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                     /clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism="Lactuca sativa"
                                                                                                                                                                                                                                                                                                                                                                                 clone="QGF25103"
                                                                                                                                                                                                                                                                                                                                                                                                                              cultivar="L.serriola"
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_LIB=QG_ABCDI lettuce salinas
_SEQ=GTTGCACGGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           _type="mRNA"
                                                                                                                                                                                                                                                                                                                                                    host="E.coli"
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Pred. No.
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Best Local S
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                                                                       Local
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            480
                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cichorieae; Lactuca.

1 (bases 1 to 223)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Leituce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGA2a06.yg.ab1 QG_ABCDI lettuce QGA2a06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactuca sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ847396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for details.
Plate: QGA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://compgenomics.ucdavis.edu,
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TTTATTAATTTATATATATTAAA 502
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                                                                                                                                                                                                                              /clone lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library size bias.
                                                                                                                                                                                                           construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                  TAG_TISSUE=roots
TAG_LIB=QG_ABCDI lettuce salinas
TAG_SEQ=GTTGCACGGG"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Salinas"
                                                                                                                                                                                                                                                                                                                                                                                                                'lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="QGA2a06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Lactuca sativa"
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100.0%; Pr
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100.0%; Pr
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; Pred. No.
                                                                     Score 23; Pred. No.
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                                                    Mismatches
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                                                                       DB 13;
23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       see http://cgpdb.ucdavis.edu/
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                                                                                          Length 223;
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RESULT 7
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AUTHORS
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VERSION
KEYWORDS
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BU013709
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Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
                BQ981419
353 bp mRNA linear EST 21-AUG-2002 QGE13L15.yg.abl QG EFGHJ lettuce serriola Lactuca sativa cDNA clone QGE13L15, mRNA sequence.
BQ981419
BQ981419 GI:22398942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
spermatophyta; Magnoliophyta; etales; Asteraceae; Cichorioideae;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
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QGJ5G07.yg.ab1 QG_EFGHJ lettuce
QGJ5G07, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bmail: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig7771, see http://cgpdb.ucdavis.edu/
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Fax: 1-(530)-752-9659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cichorieae; Lactuca.
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                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                              TAG_TISSUE=roots
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=GTTGCACGGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                         size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGJ5G07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'lab_host="E.coli"
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                                                                                                                                                                                                                                                                                                 2.1%;
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Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                 0;
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Pred. No.
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. 22;
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                                                                                                                                                                                                                                                                                                                      Length 259;
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cDNA clone
                                                                                                                                                                                                                                                                                 0
                                     REFERENCE
AUTHORS
                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                          RESULT 8
AV665533
LOCUS
DEFINITION
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COMMENT
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AUTHORS
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Best Local
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TITLE
                                                                                                                                         ORGANISM
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 TTTATTAATTTATATATATAAA 502
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                              AV665533 Bos taurus brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases i to 353)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., Van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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Establishment of a high throughput EST sequencing system using
                                                      1 (bases 1 to 432)
Takasuga, A., Hirotsune, S., Itoh, R.,
                                                                                                                                                                                                                           Bos taurus (cow)
                                                                                                                                                                                                                                                                                                             3', mRNA sequence.
AV665533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: QGE13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
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                                  and Sugimoto,Y.
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TAG_LIB-QG_EFGHJ lettuce serriola
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/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
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Location/Qualifiers
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/cultivar="L.serriola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lab_host="E.coli"
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Pred. No.
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                                                      Jitohzono, A.,
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                                                        Suzuki, H., Aso, H.
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU011575 ----- QGJ16J21.yg.abl QG EFGHJ lettuce serriola Lactuca sativa cDNA clone QGJ16J21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                      Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                     Cichorieae; Lactuca.

1 (Dases 1 to 551)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single pass sequencing.
This clone was obtained from a polyA-deleted
Location/Qualifiers
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Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTS Nucleic Acids Res. 29 (22), E108 (2001) 21570554 11713328
                                                                                                                                                                                                                                                                                      http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                      Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig7771, see http://cgpdb.uc
                                                                                                                                                                  Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU011575.1 GI:22445970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-248-25-564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshikazu
                                                                                                                                                                                                    Asmundson Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactuca sativa
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                                                                                  QGJ16 row: J
/organism="Lactuca sativa"
/mol_type="mRNA"
                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
vas deleted from a Not1 site"
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/mol_type="mRNA"
/db_xref="taxon:9913"
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lab_host="DH10B"
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"tissue_type="brain"
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Pred. No.
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                                                                                                                          see http://cgpdb.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                           Shirakawa Institute of Animal Genetics Odakura, Nishigo, Nishi-shirakawa, FukuTel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshikazu Sugimoto
Animal Genetics Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                        Email: kazusugi@cocoa.ocn.ne.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ovine ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 607)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                      le pass sequencing.
                                                                                                                                                                                                                                  clone was obtained from a polyA-deleted cDNA library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ishment of a high throughput EST sequencing syst tail-removed cDNA libraries and determination
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was deleted from a Not1 site"
            /clone="B1BR049B04"
/tlssue_type="brain"
/dev_stage="fetus"
/lab_host="pH108"
/lab_host="Bos taurus brain fetus"
/clone_lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                                           organism="Bos taurus"
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RESULT 12
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Best Local
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GSS; genome survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-APR-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National Submitted (12-APR-2000) Genoscope - Centre National BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@ge - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)
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166C04 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
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AV334716 236 bp mRNA linear EST AV334716 RIKEN full-length enriched, adult male medulla Mus musculus cDNA clone 6330563N19 3', mRNA sequence.

oblongata

Mus musculus

Mus musculus (house mouse)

GI:6374768

Eukaryota;

Eutheria;

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Mus musculus AV334716 AV334716.1 ( EST.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muzamatsu,M., Okazaki,Y. and
Hayashizaki,Y.
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Tel: 81-45-503-9222
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The Institute of Physical and Chemical Research (RIKEN)
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                        Similarity
2.0%; So ilarity 100.0%; I Conservative 0;
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                                                                                                                                 /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                  from Lambda
BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="medulla oblongata"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male medulla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain="CS7BL/6J"
Score 22; DB; Pred. No. 65; 0; Mismatches
                        65;
                                              9
  0
                                              Length 236;
    Indels
  0
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  Gaps
  0;
                          ACCESSION
VERSION
                                                                                                                RESULT 15
BQ597016
LOCUS
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AZ726944/c
LOCUS
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    KEYWORDS
                                                                                            DEFINITION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                     343
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                   BQ597016
BQ597016.1
                                                                                                                                                                                                                                                                                                                                  22;
                                                                                            BQ597016 424 bp mRNA PfESToab25f02.yl Plasmodium falciparum 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ726944 367 bp DNA linear (RPCI-24-113124.TV RPCI-24 Mus musculus genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 113 row: I column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                               falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bmail: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                        Similarity
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .367
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Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 to 367)
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/strain="C57BL/6J"
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                                                                      3D7
                                                                                                                                                                                                                                                                                                                                                      2.0%;
                                                                    cDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _type="Spleen/Brain"
e_lib="RPCI-24"
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                                                                                                                                                                                                                                                                                                                                                      Score 22; Pred. No.
                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  Mismatches
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BB
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                                                                                               linear EST 24-JUN-2002 asexual cDNA Plasmodium
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Search completed: May 26, 2004, 12:51:08 Job time : 2588.32 secs
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                     127 TTTAAAATAAAATTTTTTTAA 148
                                                                                                                                                                                                                                                                                              510 TTTAAAATAAAATTTTTTTAA 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            2.0%; Score 22; DB 13; Length 424; ilarity 100.0%; Pred. No. 55; Conservative 0; Mismatches 0; Indels
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/ (lab host="Delay (lab host="Delay
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/db_xref="taxon:36329"
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